SEQUENCE LISTING

<110> Mahajan, Pramod B.

<120> Mre11 Orthologue and Uses Thereof

<130> 1264C

<150> US 09/835,654
<151> 2001-04-16

<150> US 60/198,570
<151> 2000-04-19

<160> 9

<170> FastSEQ for Windows Version 3.0

<210> 1
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<212> DNA
<213> Zea mays

<220>
<221> CDS
<222> (151)...(1806)

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gacccacgcg tccggccggc ccttctcttc ccttgctgct gtgcgaaccc gagcgcccaa       60
acctgaactt aagctatttg gggctacttg tatttggaaa aaatatatcg ggtcctttac      120
tggtccgccg gtgttatttt aacttatgaa atg gtt ggt ttt tgc agt gca tta      174
                                  Met Val Gly Phe Cys Ser Ala Leu
                                   1               5

gat tta cag caa cgg att ggt ttg gcc aac acg ttg agt tca ggt tca      222
Asp Leu Gln Gln Arg Ile Gly Leu Ala Asn Thr Leu Ser Ser Gly Ser
    10               15                   20

atg tct gaa cca gca caa cct agt gga ggg gaa ggt gat gtc aac acg      270
Met Ser Glu Pro Ala Gln Pro Ser Gly Gly Glu Gly Asp Val Asn Thr
 25                  30                   35                   40

ctc cga ata ctt gta gca acc gac tgc cat cta ggc tac atg gag aaa      318
Leu Arg Ile Leu Val Ala Thr Asp Cys His Leu Gly Tyr Met Glu Lys
                 45                   50                   55

gat gag ata cgt agg ttt gat tcc ttt caa gca ttt gag gag att tgc      366
Asp Glu Ile Arg Arg Phe Asp Ser Phe Gln Ala Phe Glu Glu Ile Cys
             60                   65                   70

gca ttg gca gat aaa aat aag gtg gat ttt ata ctt ctc ggt ggt gat      414
Ala Leu Ala Asp Lys Asn Lys Val Asp Phe Ile Leu Leu Gly Gly Asp
         75                   80                   85
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1

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cta ttc cat gag aac aag ccg tca cgc tca acc ctg gta aaa acg att          462
Leu Phe His Glu Asn Lys Pro Ser Arg Ser Thr Leu Val Lys Thr Ile
         90              95                  100

gag att cta cgg cgc tac tgc cta aat gat caa cct gtg aag ttc cag          510
Glu Ile Leu Arg Arg Tyr Cys Leu Asn Asp Gln Pro Val Lys Phe Gln
105                     110                 115                 120

gtt gtc agt gat cag aca gtt aac ttt cca aac agg ttt ggt aag gta          558
Val Val Ser Asp Gln Thr Val Asn Phe Pro Asn Arg Phe Gly Lys Val
                125             130                 135

aat tat gaa gac cca aac ttt aac gtt ggt ctg cct gtg ttc acc att          606
Asn Tyr Glu Asp Pro Asn Phe Asn Val Gly Leu Pro Val Phe Thr Ile
                140             145                 150

cat gga aat cat gat gac cct gct gga gtg gat aat ctc tct gct atc          654
His Gly Asn His Asp Asp Pro Ala Gly Val Asp Asn Leu Ser Ala Ile
            155             160             165

gat att ctt tcg gct tgc aat ctt gta aat tat ttt gga aag atg gac          702
Asp Ile Leu Ser Ala Cys Asn Leu Val Asn Tyr Phe Gly Lys Met Asp
    170             175             180

ctt ggt ggc tct ggc gtt ggt cag ata gca gtt tat cct gta ctt gta          750
Leu Gly Gly Ser Gly Val Gly Gln Ile Ala Val Tyr Pro Val Leu Val
185                 190             195                 200

aaa aag ggc atg act tca gtt gca ctg tat ggt ctt gga aac att aga          798
Lys Lys Gly Met Thr Ser Val Ala Leu Tyr Gly Leu Gly Asn Ile Arg
                205                 210                 215

gat gaa cga cta aat aga atg ttt cag acg cct cat tca gta cag tgg          846
Asp Glu Arg Leu Asn Arg Met Phe Gln Thr Pro His Ser Val Gln Trp
            220             225             230

atg cga cct gga act caa gat ggg gag tca gcg tct gac tgg ttc aat          894
Met Arg Pro Gly Thr Gln Asp Gly Glu Ser Ala Ser Asp Trp Phe Asn
            235             240             245

ata ttg gta ctt cat cag aat agg ata aag aca aac cct aaa agt gcc          942
Ile Leu Val Leu His Gln Asn Arg Ile Lys Thr Asn Pro Lys Ser Ala
    250             255             260

atc aat gag cat ttc tta cca ggt tca tca gtc gcg acg tcc ctg att          990
Ile Asn Glu His Phe Leu Pro Gly Ser Ser Val Ala Thr Ser Leu Ile
265             270             275                 280

gat ggt gaa gca aaa cca aag cat gtt ctt ttg tta gaa atc aag gga          1038
Asp Gly Glu Ala Lys Pro Lys His Val Leu Leu Leu Glu Ile Lys Gly
                285             290             295

aat cag tac agg cca acc aaa ata cct ctg aga tct gtc aga cct ttt          1086
Asn Gln Tyr Arg Pro Thr Lys Ile Pro Leu Arg Ser Val Arg Pro Phe
                300             305             310
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2

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gaa tat gct gag gtt gtg ttg aaa gat gaa gca gat gtt aac tca aat       1134
Glu Tyr Ala Glu Val Val Leu Lys Asp Glu Ala Asp Val Asn Ser Asn
        315             320             325

gat cag gac tct gtg ctt gaa cat ttg gat aaa att gta aga aat ctg       1182
Asp Gln Asp Ser Val Leu Glu His Leu Asp Lys Ile Val Arg Asn Leu
        330             335             340

att gag aag agt agc caa cca act gcc agc aga tca gag ccc aaa ctt       1230
Ile Glu Lys Ser Ser Gln Pro Thr Ala Ser Arg Ser Glu Pro Lys Leu
345             350             355             360

cca tta gtt aga atc aag gta gat tac tct ggg ttt tca aca ata aac       1278
Pro Leu Val Arg Ile Lys Val Asp Tyr Ser Gly Phe Ser Thr Ile Asn
                365             370             375


cca caa cgt ttt ggt cag aag tat gtt gga aag gtc gca aac cct caa       1326
Pro Gln Arg Phe Gly Gln Lys Tyr Val Gly Lys Val Ala Asn Pro Gln
                380             385             390

gat att ctc att ttc tca aaa tca gca aag aag cgc cag act aca gga       1374
Asp Ile Leu Ile Phe Ser Lys Ser Ala Lys Lys Arg Gln Thr Thr Gly
        395             400             405

gat cac att gat gat tct gag aaa ctt cgt cct gag gaa cta aac caa       1422
Asp His Ile Asp Asp Ser Glu Lys Leu Arg Pro Glu Glu Leu Asn Gln
        410             415             420

caa aca atc gaa gct ctg gtc gca gag agt aac ttg aaa atg gag att       1470
Gln Thr Ile Glu Ala Leu Val Ala Glu Ser Asn Leu Lys Met Glu Ile
425             430             435             440

ctt ccg gtt gat gat ttg gac att gcg ttg cat gat ttt gtg aac aag       1518
Leu Pro Val Asp Asp Leu Asp Ile Ala Leu His Asp Phe Val Asn Lys
                445             450             455

gat gac aag atg gca ttt tat tca tgt ttg cag aga aac ctt gaa gaa       1566
Asp Asp Lys Met Ala Phe Tyr Ser Cys Leu Gln Arg Asn Leu Glu Glu
                460             465             470

acc agg aat aag ttg agt tct gaa gca gat aaa tcc aaa ttt gag gaa       1614
Thr Arg Asn Lys Leu Ser Ser Glu Ala Asp Lys Ser Lys Phe Glu Glu
                475             480             485

gaa gat ata ata gtc aaa gtt ggc gag tgc atg cag gaa cgc gtt aag       1662
Glu Asp Ile Ile Val Lys Val Gly Glu Cys Met Gln Glu Arg Val Lys
        490             495             500

gaa agg tct ctg cac tct aag gac ggc aca cgt ttg aca aca ggc tct       1710
Glu Arg Ser Leu His Ser Lys Asp Gly Thr Arg Leu Thr Thr Gly Ser
505             510             515             520

cac aac ttg gtg ttt aat tat ctg agc ctt aat atc ttt tct ttt tgt       1758
His Asn Leu Val Phe Asn Tyr Leu Ser Leu Asn Ile Phe Ser Phe Cys
```

3

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att ttt cct ggg gct gga tac tgg aca gct agt aac tct tac aac ctt      1806
Ile Phe Pro Gly Ala Gly Tyr Trp Thr Ala Ser Asn Ser Tyr Asn Leu
        540                      545                  550

taactaggat actggaggta aatcttttac agctcaaagc aaccagaact ccttcagtga    1866
tgatgaagac accagggaga tgcttcttgg tgcaagatca actgatgttg acgaaaatc     1926
atctggattt actagaccct ccaaagatac tgctgatgtt gctaaacgtg gtacttccaa    1986
aagaggcagg ggaagaggca ccagttcaat gaagcagacc actcttagtt tcagccagtc    2046
aaggtcagct accgttattc gtagtgagga tgtggcttcc tctgaggagg aagcagatgc    2106
aaatgaagtt gttgaaaatt cagaagagga gagtgcgcaa caagttggac gtaaaagagc    2166
agctcctagg ggtagaggta gaggtagagg cggaggttcc actgcaaaga gggggcgaaa    2226
aacagatatt gcttccatgc aaaatatgat gagcaaagat gatgatgatt cagaagatga    2286
accgccaaag aaaactcctc gggtcaccag gaactatggc gctgtcagga ggagatgacc    2346
ctttaaggag ttcttgctca tgagagttat aggctaggtg ttttgtcttg taaagttgga    2406
agagccgacg tgtttttatc aaccttgacg tcgaccagtt tgcgttgccg tgaactgact    2466
gtaccttgta cacgcccgaa tgtaacggat ttttgggatt tatacatcct tgtagctgct    2526
taaattccag cgattgctgt caaatgaact tcgggaaaaa aaaaaaaaaa aaaaaaaaa     2586
aaaaaaaaaa a                                                          2597
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        <211> 552
        <212> PRT
        <213> Zea mays

        <400> 2
Met Val Gly Phe Cys Ser Ala Leu Asp Leu Gln Gln Arg Ile Gly Leu
 1               5                  10                  15
Ala Asn Thr Leu Ser Ser Gly Ser Met Ser Glu Pro Ala Gln Pro Ser
            20              25                  30
Gly Gly Glu Gly Asp Val Asn Thr Leu Arg Ile Leu Val Ala Thr Asp
        35              40                  45
Cys His Leu Gly Tyr Met Glu Lys Asp Glu Ile Arg Arg Phe Asp Ser
    50              55                  60
Phe Gln Ala Phe Glu Glu Ile Cys Ala Leu Ala Asp Lys Asn Lys Val
65              70                  75                  80
Asp Phe Ile Leu Leu Gly Gly Asp Leu Phe His Glu Asn Lys Pro Ser
            85                  90                  95
Arg Ser Thr Leu Val Lys Thr Ile Glu Ile Leu Arg Arg Tyr Cys Leu
            100                 105                 110
Asn Asp Gln Pro Val Lys Phe Gln Val Val Ser Asp Gln Thr Val Asn
            115                 120                 125
Phe Pro Asn Arg Phe Gly Lys Val Asn Tyr Glu Asp Pro Asn Phe Asn
    130                 135                 140
Val Gly Leu Pro Val Phe Thr Ile His Gly Asn His Asp Asp Pro Ala
145                 150                 155                 160
Gly Val Asp Asn Leu Ser Ala Ile Asp Ile Leu Ser Ala Cys Asn Leu
            165                 170                 175
Val Asn Tyr Phe Gly Lys Met Asp Leu Gly Gly Ser Gly Val Gly Gln
            180                 185                 190
Ile Ala Val Tyr Pro Val Leu Val Lys Lys Gly Met Thr Ser Val Ala
    195                 200                 205
Leu Tyr Gly Leu Gly Asn Ile Arg Asp Glu Arg Leu Asn Arg Met Phe
    210                 215                 220
Gln Thr Pro His Ser Val Gln Trp Met Arg Pro Gly Thr Gln Asp Gly
```

4

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225                     230                     235                     240
Glu Ser Ala Ser Asp Trp Phe Asn Ile Leu Val Leu His Gln Asn Arg
                245                     250                     255
Ile Lys Thr Asn Pro Lys Ser Ala Ile Asn Glu His Phe Leu Pro Gly
                260                     265                     270
Ser Ser Val Ala Thr Ser Leu Ile Asp Gly Glu Ala Lys Pro Lys His
                275                     280                     285
Val Leu Leu Leu Glu Ile Lys Gly Asn Gln Tyr Arg Pro Thr Lys Ile
            290                     295                     300
Pro Leu Arg Ser Val Arg Pro Phe Glu Tyr Ala Glu Val Val Leu Lys
305                     310                     315                     320
Asp Glu Ala Asp Val Asn Ser Asn Asp Gln Asp Ser Val Leu Glu His
                325                     330                     335
Leu Asp Lys Ile Val Arg Asn Leu Ile Glu Lys Ser Ser Gln Pro Thr
                340                     345                     350
Ala Ser Arg Ser Glu Pro Lys Leu Pro Leu Val Arg Ile Lys Val Asp
                355                     360                     365
Tyr Ser Gly Phe Ser Thr Ile Asn Pro Gln Arg Phe Gly Gln Lys Tyr
            370                     375                     380
Val Gly Lys Val Ala Asn Pro Gln Asp Ile Leu Ile Phe Ser Lys Ser
385                     390                     395                     400
Ala Lys Lys Arg Gln Thr Thr Gly Asp His Ile Asp Asp Ser Glu Lys
                405                     410                     415
Leu Arg Pro Glu Glu Leu Asn Gln Gln Thr Ile Glu Ala Leu Val Ala
            420                     425                     430
Glu Ser Asn Leu Lys Met Glu Ile Leu Pro Val Asp Asp Leu Asp Ile
            435                     440                     445
Ala Leu His Asp Phe Val Asn Lys Asp Asp Lys Met Ala Phe Tyr Ser
        450                     455                     460
Cys Leu Gln Arg Asn Leu Glu Glu Thr Arg Asn Lys Leu Ser Ser Glu
465                     470                     475                     480
Ala Asp Lys Ser Lys Phe Glu Glu Glu Asp Ile Ile Val Lys Val Gly
                485                     490                     495
Glu Cys Met Gln Glu Arg Val Lys Glu Arg Ser Leu His Ser Lys Asp
                500                     505                     510
Gly Thr Arg Leu Thr Thr Gly Ser His Asn Leu Val Phe Asn Tyr Leu
            515                     520                     525
Ser Leu Asn Ile Phe Ser Phe Cys Ile Phe Pro Gly Ala Gly Tyr Trp
        530                     535                     540
Thr Ala Ser Asn Ser Tyr Asn Leu
545                     550
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<210> 3
<211> 36
<212> DNA
<213> Artificial Sequence

<220>
<223> Designed oligonucleotide based upon an adaptor
      used for cDNA library construction and poly(dT) to
      remove clones which have a poly(A) tail but no
      cDNA insert.

<400> 3
tcgacccacg cgtccgaaaa aaaaaaaaaa aaaaaa   36

<210> 4
<211> 2308
<212> DNA
<213> Zea mays

<400> 4

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catttgagga gatttgcgca ttggcagata aaaataaggt ggattttata cttctcggtg     120
gtgatctatt ccatgagaac aagccgtcac gctcaaccct ggtaaaaacg attgagattc     180
tacggcgcta ctgcctaaat gatcaacctg tgaagttcca ggttgtcagt gatcagacag     240
ttaactttcc aaacaggttt ggtaaggtaa attatgaaga cccaaacttt aacgttggtc     300
tgcctgtgtt caccattcat ggaaatcatg atgaccctgc tggagtggat aatctctctg     360
ctatcgatat tctttcggct tgcaatcttg taaattattt tggaaagatg gaccttggtg     420
gctctggcgt tggtcagata gcagtttatc ctgtacttgt aaaaaagggc atgacttcag     480
ttgcactgta tggtcttgga aacattagag atgaacgact aaatagaatg tttcagacgc     540
ctcattcagt acagtggatg cgacctggaa ctcaagatgg ggagtcagcg tctgactggt     600
tcaatatatt ggtacttcat cagaatagga taaagacaaa ccctaaaagt gccatcaatg     660
agcatttctt accaggttca tcagtcgcga cgtccctgat tgatggtgaa gcaaaaccaa     720
agcatgttct tttgttagaa atcaagggaa atcagtacag gccaaccaaa atacctctga     780
gatctgtcag acctttttgaa tatgctgagg ttgtgttgaa agatgaagca gatgttaact     840
caaatgatca ggactctgtg cttgaacatt tggataaaat tgtaagaaat ctgattgaga     900
agagtagcca accaactgcc agcagatcag agcccaaact tccattagtt agaatcaagg     960
tagattactc tgggttttca acaataaacc cacaacgttt tggtcagaag tatgttggaa    1020
aggtcgcaaa ccctcaagat attctcattt tctcaaaatc agcaaagaag cgccagacta    1080
caggagatca cattgatgat tctgagaaac ttcgtcctga ggaactaaac caacaaacaa    1140
tcgaagctct ggtcgcagag agtaacttga aaatggagat tcttccggtt gatgatttgg    1200
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agagaaacct tgaagaaacc aggaataagt tgagttctga agcagataaa tccaaatttg    1320
aggaagaaga tataatagtc aaagttggcg agtgcatgca ggaacgcgtt aaggaaaggt    1380
ctctgcactc taaggacggc acacgtttga caacaggctc tcacaacttg gtgtttaatt    1440
atctgagcct taatatcttt tcttttttgta ttttttcctgg ggctggatac tggacagcta    1500
gtaactctta caacctttaa ctaggatact ggaggtaaat cttttacagc tcaaagcaac    1560
cagaactcct tcagtgatga tgaagacacc agggagatgc ttcttggtgc aagatcaact    1620
gatgttggac gaaaatcatc tggatttact agaccctcca aagatactgc tgatgttgct    1680
aaacgtggta cttccaaaag aggcagggga agaggcacca gttcaatgaa gcagaccact    1740
cttagtttca gccagtcaag gtcagctacc gttattcgta gtgaggatgt ggcttcctct    1800
gaggaggaag cagatgcaaa tgaagttgtt gaaaattcag aagaggagag tgcgcaacaa    1860
gttggacgta aaagagcagc tcctaggggt agaggtagag gtagaggcgg aggttccact    1920
gcaaagaggg ggcgaaaaac agatattgct tccatgcaaa atatgatgag caaagatgat    1980
gatgattcag aagatgaacc gccaaagaaa actcctcggg tcaccaggaa ctatggcgct    2040
gtcaggagga gatgacccct taaggagttc ttgctcatga gagttatagg ctaggtgttt    2100
tgtcttgtaa agttggaaga gccgacgtgt ttttatcaac cttgacgtcg accagtttgc    2160
gttgccgtga actgactgta ccttgtacac gcccgaatgt aacggatttt tgggatttat    2220
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aaaaaaaaaa aaaaaaaaaa aaaaaaaa                                       2308
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<210> 5
<211> 396
<212> DNA
<213> Zea mays

<400> 5

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tcgacccacg cgtccggccg gcccttctct tcccttgctg ctgtgcgaac ccgagcgccc      60
aaacctgaac ttaagctatt tggggctact tgtatttgga aaaaatatat cgggtccttt     120
actggtccgc cggtgttatt ttaacttatg aaatggttgg tttttgcagt gcattagatt     180
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6

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tacagcaacg gattggtttg gccaacacgt tgagttcagg ttcaatgtct gaaccagcac       240
aacctagtgg aggggaaggt gatgtcaaca cgctcctaat acttgtagca accgactgcc       300
atctaggcta catggagaaa gatgagatac gtaggtttga ttcctttcaa gcatttgagg       360
agatttgcgc attggcagat aaaaataagg tggatt                                 396
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        <210> 6
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        <212> DNA
        <213> Artificial Sequence

        <220>
        <223> M13R synthetic primer

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agcggataac aatttcacac aggaaacagc tatgac                                   36


        <210> 7
        <211> 20
        <212> DNA
        <213> Artificial Sequence

        <220>
        <223> R1 synthetic primer

        <400> 7
cttattttta tctgccaatg                                                     20


        <210> 8
        <211> 25
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        <213> Artificial Sequence

        <220>
        <223> T7 synthetic primer

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taatacgact cactataggg cgaat                                               25


        <210> 9
        <211> 20
        <212> DNA
        <213> Artificial Sequence

        <220>
        <223> R2 synthetic primer

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gcgtgacggc ttgttctcat                                                     20
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